Patent

Attorney's Docket No. 032266-003

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

VON SCHAEWEN, Antje

Application No.: 09/591,466

Filed: June 9, 2000

For:
Plant GntI sequences and the use thereof for the production of plants having reduced or lacking N-acetyl glucosaminyl transferase I (GntI) activity

Group Art Unit: 1655

Examiner: J. Goldberg

AMENDMENT AND REPLY TO OFFICE ACTION

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

This Amendment and Reply to Office Action is submitted in response to the Office Action mailed December 21, 2001, for the above-referenced application. The Examiner set a three (3) month period for response. A petition requesting a one (1) month extension of time accompanies this response which is being filed on or before its current due date of April 22, 2002 (April 21, 2002 being a Sunday).

AMENDMENT

In the Specification:

Please make the following amendments in the specification. Pursuant to 37 C.F.R. §1.121(b)(1)(iii), a marked-up copy of the amended paragraphs in the specification is attached herewith on separate pages.

Please replace the paragraph starting at page 28, line 18 with the following:

B1 -- Fig. 2: Full length cDNA sequence (SEQ ID NO:1) of a plant GnTI from potato (*Solanum tuberosum* L.) and amino acid sequence deduced therefrom (SEQ ID NO:2). By way of example, the complete cDNA of the membrane anchor containing *GntI* isoform from potato leaf tissue (A1) is illustrated. The EcoRI/NotI linkers at the 5' and 3' ends of the cDNA are highlighted by bold letters, the binding sites of the degenerate oligonucleotides used for obtaining the RT-PCR probe are underlined. In contrast to already published animal GnTI sequences, the protein sequence derived from the potato cDNA clones contains a potential N-glycosylation site: Asn-X (without Pro)-Ser/Thr, which is indicated by an asterisk. The region of the membrane anchor is highlighted in italics (aa 10 to 29). The start of the isoform (A8), which is potentially located in the cytosol, is indicated by an arrow.--

Please replace the paragraph starting at page 29, line 6 with the following:

B2 -- B, Comparison of the derived amino acid sequences of different plant *GntI*-cDNA clones. A_Stb-A1 (SEQ ID NO:2), GnTI from potato leaf; B_Ntb-A9 (SEQ ID NO:4), GnTI from tobacco leaf (A9); C_Atb-Full (SEQ ID NO:6), GnTI from *Arabidopsis thaliana*. Identical aa are highlighted in black, similar aa in light grey.--

Please replace the paragraph starting at page 31, line 16 with the following:

B3 -- Total RNA was isolated from potato and tobacco leaf tissue, and cDNA fragment of about 90 bp were amplified by means of RT-PCR in combination with degenerate primers (procedure analogous to ref. 31), which were derived from conserved amino acid regions of known GnTI sequences from animal organisms (sense primer 1* (SEQ ID NO:7), 5'-TG(CT) G(CT)I (AT) (GC) I GCI TGG (AC)A(CT) GA(CT) AA(CT) -3'; antisense primer 3* (SEQ ID NO:8), 5' -CCA ICC IT(AG) ICC (ACGT)G(CG) (AG)AA (AG)AA (AG)TC-3'; 30 pmol of each primer per 50 µl PCR assay at an annealing temperature of 55°C and 45 cycles). Following gel elution, the ends of the PCR products were repaired (i.e. blunt ended using DNA polymerase I and phosphorylated using T4 polynucleotide kinase) and clones into the EcoRV restriction site of pBSK (Stratagene).

By comparison with known GnTI sequences between the primers (arrows), the identity of the derived amino acid sequences from the potato and tobacco RT-PCR products could be confirmed as being homologous; ⇒Q(R/M)QFVQDP(D/Y)ALYRS (SEQ ID NO:9)⇐ (homologous aa are underlined). Of one clone each, radiolabelled probes were synthesized by means of PCR (standard PCR assay using degenerate primers as above, nucleotide mixture without dCTP, but instead with 50 μCi α-^{32}P-dCTP [>3000 Ci/mMol]), and different cDNA libraries were screened for *GntI* containing clones using the corresponding homologous potato or tobacco probes, respectively (procedure analogous to ref. 31; the stringent hybridization conditions have already been described in the text above). The cDNA libraries were prepared from mRNA of young and still growing plant parts (sink tissues). Following cDNA synthesis and ligating EcoRI/NotI adaptors (cDNAsynthesis kit, Pharmacia) EcoRI compatible lambda arms were ligated, those packaged and used to transfect *E. coli* XL1 Blue cells (Lambda ZAPII cloning and packaging system, Stratagene). Following amplification of the libraries, one full-length *GntI* clone each was isolated from a potato leaf sink library (A1 according to Fig. 2 and SEQ ID NO: 1) and a tobacco leaf sink library (A9 according to SEQ ID NO: 3), as well as two additional clones from a tuber sink library (A6, A8). The deduced GnTI amino-acid sequences contain a potential N-glycosylation site, Asn-X (without Pro)-Ser/Thr, in contrast to those of animals. One of the tuber *GntI* cDNA sequences carries stop condons in all three reading frames in front of the first methionine (A8). The coding region shows high homology to the longer tuber clone (A6) (only 2 aa substitutions), but displays a completely different 5' non-translated region. Furthermore, the membrane anchor characteristic for the Golgi enzyme is missing, so that this GnTI isoform might be located in the cytosol. Sequence comparisons carried out by means of the gap or pileup option, respectively, and the box option of the gcg software package (J. Devereux, P. Haeberli, O. Smithies (1984) Nucl. Acids Res. 12: 387-395) indicate, that the deduced plant GnTI amino-acid sequences exhibit only 30-40% identity and 57-59% similarity to those of animal organisms (Fig. 3A), while they are highly homologous among each other (75-90% identity, Fig. 3B). --

Please replace the paragraph starting at page 32, line 39 with the following:

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-- The procedure in the case of *Arabidopsis thaliana* was analogous, wherein for the preparation of a specific probe first a partial *GntI* sequence was amplified by RT-PCR using *GntI* sense primer 4A (SEQ ID NO:10; 5'-ATCGGAAAGCTTGGATCC CCA GTG GC(AG) GCT GTA GTT GTT ATG GCT TGC -3'; HindIII restriction site underlined, BamHI printed in bold) and antisense primer 3*, as defined above. First, a 5'-incomplete cDNA clone was isolated from a phage library (Lambda Uni-Zap) using this probe. By means of a vector insert PCR, the missing 5'-terminus was amplified from another library (via a unique SpeI restriction site in the 5' region) and assembled to yield a full-length cDNA sequence. The nucleic acid sequence determined by means of sequencing is listed in SEQ ID NO: 5.--

Please replace the paragraph starting at page 34, line 5 with the following:

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-- Into the SalI restriction site of the polylinker region (corresponding to the one of pUC18) of plant expression vector pA35 (ref. 29), a NotI linker was introduced subsequently to the fill-in of the ends (=pA35N), and the complete A1-*GntI*-cDNA (nucleotides 9 to 1657, according to the cDNA in Fig. 2) was inserted into pA35N *via* NotI (sense construct pA35N-A1s and antisense construct pA35N-Alas, respectively). The expression cassettes of the sense and antisense construct, respectively, were isolated via the terminal restriction sites (filled-in NcoI restriction site, partial post digestion with HindIII) as a fragment of about 2410 bp and inserted into the EcoRI (filled-in) and HindIII restriction sites of the binary vector pBin19 (Ref. 30) (=pBin-35-Als and pBin-35-Alas, respectively). The EcoRI restriction site of the vector is restored by fusion with the equally filled-in NcoI restriction site of the fragment. By means of a standard PCR assay (sense primer (SEQ ID NO: 11): KS sequencing primer (Stratagene) extended for PCR, 5'-GGC CCC CCC TCG AGG TCG ACG GTA TCG-3'; antisense primer (SEQ ID NO: 12): 5'-GGGCCTCTAGA*CTCGAG* AGC (CT)AC TAC TCT TCC TTG CTG CTG GCT AAT CTT G-3', XbaI restriction site underlined, XhoI restriction site in italics), there was additionally amplified a 5'-fragment of the *GntI* cDNA at an annealing temperature of 50°C (nucleotides 9 to 261, according to the cDNA in Fig. 2 and SEQ ID

NO: 1). The PCR product was digested with XbaI (within the antisense primer) and NotI (within the 5'-linker of the cDNA), isolated as a fragment of about 260 bp and cloned into pA35N (=pA35N-Al-short). The expression cassette of the short antisense construct was also inserted into pBin19 (=pBin-35-A1-short) as a EcoRI/HindIII fragment (about 1020 bp).--

B4 cont'd

Please replace the paragraph starting at page 35, line 41 and continuing into page 36, line 30 with the following:

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-- Recombinant GnTI carrying 10 additional N-terminal histidine residues (His-tag) was produced in *E. coli* by means of the pET system (Novagen) and purified by metal-chelate affinity chromatography. A cDNA fragment comprising nucleotides 275-1395 of the potato *GntI* cDNA (corresp. to aa 75-446, Fig. 2 and SEQ ID NO: 1 and 2, respectively) was amplified by standard PCR (annealing temperature of 50°C, 30 cycles , ref. 31) (sense primer *GntI*-5' fus (SEQ ID NO: 13): 5'-CATGGATCC CTC GAG AAG CGT CAG GAC CAG GAG TGC CGG C-3'; antisense primer *GntI*-3' stop (SEQ ID NO: 14): 5'-ATCCCGGGATCCG *CTA* CGT ATC TTC AAC TCC AAG TTG-3'; XhoI and BamHI restriction sites, respectively, are underlined, stop codon in italics), and inserted into vector pET16b (Novagen) (=pET-His-Al) *via* the restriction sites of the synthetic primer (5'-XhoI-*GntI*-BamHI-3'). Following propagation and analysis in *E. coli* XL1-Blue (Stratagene) the construct was stored as a glycerol culture. Competent *E. coli* BL21 (DE3) pLysS cells (Novagen) were transformed with pET-His-Al for overexpression. Addition of IPTG (Isopropyl-1-thio-β-D-galactopyranoside, at 0.5-2 mM) to a BL21 culture in logarithmic growth phase, initially induces the expression of T7 RNA polymerase (from the bacterial chromosome), and thus, also the expression of the recombinant fusion protein under control of the T7 promoter in pET vectors (Novagen). By means of metal-chelate chromatography using TALON matrix (Clontech), recombinant potato GnTI was purified from induced BL21:pET-His-Al cells under denaturating conditions *via* its His-tag (manufacturer's protocol, Novagen), and the preparation was verified with respect to homogeneity by means of SDS-PAGE.--

Please replace the existing sequence listing with the new sequence listing enclosed herewith.

In the Claims:

Please delete claims 41-46 without prejudice or disclaimer to Applicant's filing one or more continuation or divisional applications directed to the canceled subject matter.

Please amend claims 2, 31 and 47-48 so that after the amendments, the following claims are pending in this application:

2. (amended) Method according to claim 31, characterized in that for transformation an antisense or sense construct with respect to one of the cDNAs encoding N-acetyl glycosaminyl transferase I isolated from Solanum tuberosum, Nicotiana tabacum or Arabidopsis thaliana is used.

3. Method according to claim 2, characterized in that for transformation an antisense or sense construct with respect to one of the DNA sequences given in SEQ ID NO: 1, 3 or 5 is used.

31. (amended) A method for the production of glycoproteins displaying $GlcNac_2Man_5$-residues, comprising

(a) cultivating a transgenic plant, parts of transgenic plants or transformed plant cells, wherein

(i) the transgenic plant, parts of transgenic plants or transformed plant cells, respectively, is/are transformed with an antisense construct or a sense construct;

(ii) the antisense construct or sense construct comprises an antisense DNA or a sense DNA with respect to the DNA of claim 35 or a part thereof, wherein transformation of said antisense or sense construct

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results in elimination or reduction of the activity of said N-acetyl glucosaminyl transferase in said transgenic plant, parts of transgenic plants or transformed plant cells; and

(iii) the antisense or sense construct optionally contains additional regulatory sequences for the transcription of the respective antisense or sense DNA;

and

(b) isolating the desired glycoprotein from the cultivated transgenic plant, parts of transgenic plants or transformed plant cells.

32. The method according to claim 31, characterized in that the transgenic plant used is additionally transformed with the gene encoding the desired glycoprotein.

33. The method according to claim 2, characterized in that the transgenic plant used is additionally transformed with the gene encoding the desired glycoprotein.

34. The method according to claim 3, characterized in that the transgenic plant used is additionally transformed with the gene encoding the desired glycoprotein.

B3 35. (amended) An isolated DNA, comprising a DNA molecule encoding a sequence or the complementary thereof, which is selected from the group consisting of:

SEQ ID NOs:1, 3 and 5;

a DNA sequence encoding the amino acid sequence of SEQ ID Nos: 2, 4 or 6;

a DNA sequence sharing a nucleotide identity of at least 70% with SEQ ID NOs:1, 3 or 5;

a DNA sequence encoding an amino acid sequence which shares an amino acid sequence of at least 75% with SEQ ID NOs:2, 4 or 6;

a DNA sequence which hybridizes under stringent conditions to SEQ ID NOs:1, 3 or 5, or the complementary thereof; and

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a DNA sequence which hybridizes under stringent conditions to a DNA sequence, or the complementary thereof, which encodes SEQ ID NOs:2, 4 or 6.

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36. An isolated DNA which encodes a polypeptide having N-acetyl glucosaminyl transferase I activity and which hybridizes under stringent conditions to a DNA of claim 35.

37. A DNA construct comprising the DNA of claim 35 in the sense or anti-sense orientation.

38. A DNA construct comprising the DNA of claim 36 in the sense or anti-sense orientation.

39. A microorganism transformed with the DNA construct of claim 37.

40. A microorganism transformed with the DNA construct of claim 38.

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47. (amended) A transgenic plant, transgenic seed, transgenic reproduction material, part of a transgenic plant or transformed plant cell, obtainable by

(a) integration of one or more antisense or sense DNA of claim 35 under the control of a promoter effective in plants, into the genome of a plant, or

(b) viral infection by means of a virus containing one or more antisense or sense DNA of claim 35, for an extrachromosomal propagation and transcription of the antisense construct(s) in the plant tissue infected.

48. (amended) A transgenic plant, transgenic seed, transgenic reproduction material, part of a transgenic plant or transformed plant cell, obtainable by

(a) integration of one or more antisense or sense DNA of claim 36 under the control of a promoter effective in plants, into the genome of a plant, or

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(b) viral infection by means of a virus containing one or more antisense or sense DNA of claim 36, for an extrachromosomal propagation and transcription of the antisense construct(s) in the plant tissue infected.

Pursuant to 37 C.F.R. §1.121(c)(1)(ii), a marked-up copy of the amended claims is attached herewith on separate pages.

REMARKS

It is respectfully requested that this application be reconsidered in view of the above amendments and the following remarks and that all of the claims remaining be allowed.

Amendments to the Specification:

The specification has been amended to insert "SEQ ID NO"s into the description of Figures 2 and 3B, and Examples 1, 3 and 5. The specification has been further amended by replacing the existing sequence listing with a revised sequence listing that contains the newly inserted SEQ ID NOs. These sequences are disclosed in the original specification, and the only amendments are the insertions of "SEQ ID NO"s.

Accordingly, no new matter has been added by these amendments. The Examiner is hereby requested to enter these amendments.

Claims Amendments:

Claims 41-46 have been canceled without prejudice or disclaimer as non-selected claims. Applicant reserves the right to pursue prosecution of the subject matters of the canceled claims in this or future continuation and/or divisional application(s).

Claim 2 has been amended to recite "isolated from" instead of "from" to further clarify the source of the DNA.

Claim 31 has been reorganized for clarity.

Claim 25 has been amended to recite "a DNA sequence sharing a nucleotide identity of at least 70% with SEQ ID NOs:1, 3 or 5" as well as "a DNA sequence encoding an amino acid sequence which shares an amino acid sequence of at least 75% with SEQ ID

NOs:2, 4 or 6". Support for these recitations can be found, for example, at page 22, last paragraph, and page 32, lines 27-36, respectively.

Claims 47 and 48 have been amended for clarity by separating two phrases and inserting the headings of (a) and (b) before the two phrases.

No new matter has been added by these amendments. The Examiner is hereby requested to enter these amendments.

Applicant wishes to point out that the amendments presented herein are made merely in consistence with Applicant's election of claims in response to the restriction requirement or to clarify the claimed subject matter, and not to distinguish over any prior art. Thus, Applicant submits that none of the claims now presented or previously presented are obvious over the prior art.

Sequence Rules

The Office Action indicates that the present application is not in compliance with the sequence rules (with respect to the sequences disclosed in Figure 2 and 3B and the primers disclosed on, for example, 31 and 32). The specification has been amended as required, and a revised sequence listing (both paper copy and computer readable form) is enclosed herewith. The content of this sequence listing paper copy is identical to that of the computer readable form, and contains no new matter.

Therefore, Applicant submits that the present application is in compliance with the sequence rules.

Rejection Under 35 U.S.C. §112:

The rejection of claims 2, 31-35, 37, 39 and 47-48 under 35 U.S.C. §112, first paragraph as allegedly containing subject matter which was not adequately described in the specification has been obviated-in-part and traversed-in-part as set forth below.

1. The rejection of claims 35, 37, 39 and 47-48 is respectfully traversed. As the Office Action pointed out on page 4, the Federal Circuit held that an adequate written description of a DNA required a precise definition, such as by structure, formula, chemical name, or physical properties. *The Regents of the University of California v. Eli Lilly*, 43 USPQ2d 1398 (CAFC 1997).

Claim 35, either original or amended, meets this requirement. The amended claim 35 is directed to an isolated DNA comprising a DNA molecule encoding a sequence or the complementary thereof, which is selected from the group consisting of:

> SEQ ID NOs:1, 3 and 5;
>
> a DNA sequence encoding the amino acid sequence of SEQ ID Nos: 2, 4 or 6;
>
> a DNA sequence sharing a nucleotide identity of at least 70% with SEQ ID NOs:1, 3 or 5;
>
> a DNA sequence encoding an amino acid sequence which shares an amino acid sequence of at least 75% with SEQ ID NOs:2, 4 or 6;
>
> a DNA sequence which hybridizes under stringent conditions to SEQ ID NOs:1, 3 or 5, or the complementary thereof; and
>
> a DNA sequence which hybridizes under stringent conditions to a DNA sequence, or the complementary thereof, which encodes SEQ ID NOs:2, 4 or 6.

SEQ ID Nos: 1-6 are disclosed in the specification. Methods of determining the degree of sequence identity to a disclosed sequence are well known in the art, as well as

disclosed in the present specification, for example, at page 32, lines 27-31. The term "stringent conditions" is defined, as noted by the Office Action, on page 10 of the specification. Therefore, claim 35 is directed to DNA molecules that are clearly delineated with both structural features and physical properties, and any person of ordinary skill in the art can recognize that Applicant had possession of the claimed subject matter at the time of filing of the present application. If the Examiner believes that a functional feature must be recited in the claim in addition to structural features, Applicant respectfully requests a citation of the law in this regard.

Claims 37, 39 and 47-48 depend, directly or indirectly, from claim 35. Therefore, Applicant submits that they also meet the written description requirement.

2. The rejection of claims 2 and 31-34 has been obviated-in-part and traversed-in-part for the following reasons.

Claim 31 has been amended to recite "the DNA of claim 35". As discussed above, claim 35 satisfies the written description requirement. Therefore, Applicant submits that claim 31, as well as its dependent claims 2 and 32-34, also meets the written description requirement.

The Office Action stated that Applicant has not described Solanum tuberosum nucleic acids encoding N-acetyl glucosaminyl transferase I (GntI), provided how to identify that a GntI sequence is from potato origin as opposed to other origins, or demonstrated written description of any plant or potato GntI polypeptide (page 6 of the Office Action). Applicant does not completely understand these statements but wishes to point out that the GntI nucleic acid sequence of Solanum tuberosum has been disclosed as SEQ ID NO:1, and potato GntI polypeptide sequence has been disclosed as SEQ ID NO:2. The specification provides adequate guidance as to how to isolate and identify the GntI gene or polypeptide sequences from any plant, for example, in Example 1. Out of ultimate caution, Applicant has amended claim 2 to recite "isolated from" rather than "from" to indicate the origin of

each sequence encompassed in the claim. Applicant submits that any person of ordinary skilled in the art can recognize that Applicant had possession of the claimed subject matter at the time of filing of the present application.

Accordingly, withdrawal of this rejection is respectfully requested.

Rejection Under 35 U.S.C. §112:

The rejection of claims 2-3, 31-34, 37-40 and 47-48 under 35 U.S.C. §112, first paragraph as allegedly not enabled is respectfully traversed.

The Office Action questioned the use of antisense constructs in the claimed invention. As described throughout the specification (for example, at page 5, last paragraph), the present application discloses a method of reducing or eliminating GntI activities in a plant so that glycoproteins produced by the plant will display $Man_5GlcNac_2$, which has low antigenic potential. This method was enabled by Applicant's cloning for the first time the nucleic acid sequences for plant GntI genes, which encode enzymes that process the first step of converting $Man_5GlcNac_2$ to complex carbohydrate structures. Methods of reducing or eliminating gene expression using antisense constructs are well established in the art. Since plant GntI sequences are now made available by the present application, the use of antisense constructs as claimed in claims 2-3, 31-34, 37-40 and 47-48 is fully enabled.

Applicant also wishes to point out that the use of sense constructs in this respect is enabled as well. As disclosed in the specification (for example, at page 21, last paragraph), it is known in the art that a sense construct can lead to a hybridization phenomenon which affects or prevents translation of the GntI gene. Therefore, sense constructs can also result in the reduction or elimination of the GntI activity in plants.

The Office Action further stated that undue experimentation would allegedly be required to screen for additional plant GntI genes. Applicant respectfully disagrees.

As an initial matter, the USPTO bears the burden of establishing a prima facie case of non-enablement. It is incumbent upon the USPTO to explain why it doubts the truth or accuracy of any statement in a supporting disclosure and to back up assertions of its own with acceptable evidence or reasoning which is inconsistent with the contested statement. In re Bowen, 181 USPQ 48, 51 (CCPA 1974). The Office Action does not offer any explanation why undue experimentation would be required to screen for additional plant GntI genes.

In addition, a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed. *In re Wands*, 8 USPQ 2d 1401, 1404 (Fed. Cir. 1988).

In re Wands involves the make and use of monoclonal antibodies, and the court decided that it is not undue experimentation to make and screen hundreds of hybridoma clones at a time, and to repeat this process, until a clone with the desired characteristic is found. In the present application, the methods and primers for isolating plant GntI clones, as well as full-length GntI DNA sequences from three different genuses, are provided (e.g., Example 1). The specification further discloses assay methods for determining GntI enzymatic activities (e.g., page 6, third paragraph) and methods of complementing GntI mutant plants with potential clones (e.g., Example 2). Therefore, the specification provides sufficient guidance, including working examples, with respect to the direction in which the experimentation should proceed. No undue experimentation is required under *in re Wands*.

Accordingly, Applicant respectfully requests that this rejection be withdrawn.

Rejection Under 35 U.S.C. §112, Second Paragraph:

The rejections of claims 2-3 and 31-34 under 35 U.S.C. §112, second paragraph, as allegedly being indefinite have been obviated for the following reasons.

A) The term "minimal, uniform" has been deleted from the rejected claims. Furthermore, claim 31 has been rewritten to clarify the claim language.

B) Claims 32-34 have been clarified due to rewriting of claim 31. Thus, claims 31, 2 and 3 recite methods of using a GntI construct to produce desired glycoproteins, without specifying the source of the glycoprotein genes. Claims 32-34, depending from claims 31, 2 and 3, respectively, further recite that the gene coding for the glycoprotein has been transformed into the plant.

C) Claims 47 and 48 have been amended to clearly describe the claimed subject matter. Applicant respectfully submits that the rewritten claims are not confusing.

Consequently, withdrawal of these rejections is respectfully requested.

Rejection Under 35 U.S.C. §102:

The rejection of claims 31-32 under 35 U.S.C. §102 in view of Gomez et al. (PNAS 91:1829-1833) has been obviated for the reasons set forth below.

The standard of anticipation under 35 U.S.C. §102 is that each and every element of the claim must be found in the cited reference. In re Marshall (CCPA 1978), 198 USPQ 344.

Claim 31, as amended, is directed to a method for the production of glycoproteins displaying $GlcNac_2Man_5$-residues, comprising

(a) cultivating a transgenic plant, parts of transgenic plants or transformed plant cells, wherein

(i) the transgenic plant, parts of transgenic plants or transformed plant cells, respectively, is/are transformed with an antisense construct or a sense construct;

(ii) the antisense construct or sense construct comprises an antisense DNA or a sense DNA with respect to the DNA of claim 35 or a part thereof, wherein transformation of said antisense or sense construct results in elimination or reduction of the activity of said N-acetyl glucosaminyl transferase in said transgenic plant, parts of transgenic plants or transformed plant cells; and

(iii) the antisense or sense construct optionally contains additional regulatory sequences for the transcription of the respective antisense or sense DNA;

and

(b) isolating the desired glycoprotein from the material cultivated.

In contrast, Gomez et al. teaches a method of restoring the GntI activity of a mutant plant with the human GntI gene. Thus, Gomez et al. do not teach the use of a plant GntI sequence, or a homolog thereof, to reduce or eliminate the GntI activity in a plant. Therefore, Gomez et al. do not teach each and every element of claim 31.

Claim 32 depends from claim 31 and recites all the elements of claim 31. Likewise, Gomez et al. do not teach each and every element of claim 32.

For the reasons articulated above, withdrawal of this rejection is respectfully requested.

Allowable Subject Matter

Applicant noticed that original claim 36 stands clear of any rejection or objection. Therefore, Applicant respectfully submits that original claim 36 is allowable. Claim 35, from which claim 36 depends, has been amended, and therefor claim 36 has been indirectly amended. However, since claim 35 is in condition for allowance as articulated above, Applicant submits that the amended claim 36 is also allowable.

Conclusions:

For the reasons set forth above, Applicant submits that the claims of this application are patentable. Reconsideration and withdrawal of the Examiner's rejections are hereby requested. Allowance of the claims remaining in this application is earnestly solicited.

In the event that a telephone conversation could expedite the prosecution of this application, the Examiner is requested to call the undersigned at (650) 622-2340.

Respectfully submitted,

BURNS, DOANE, SWECKER & MATHIS, L.L.P.

By: _____

Ping F. Hwung
Registration No. 44,164
Attorney for Applicant
Redwood Shores, CA Office
(650) 622-2300

P.O. Box 1404
Alexandria, Virginia 22313-1404
Date: April 12, 2002